

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 13, 2001, 13:40:10 ; Search time 17.41 Seconds

(without alignments)
2305.801 Million cell updates/sec

Title: US-09-784-340-2

Perfect score: 527

Sequence: 1 MRSDKSLVFLLLQLPFCVGC.....KCFLESCQKFKTKRIEKRE 527

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR68:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	7.6	527	2	SI5089
2	33	6.3	528	2	JN0619
3	29	5.5	529	2	A42233
4	28	5.3	528	2	JN0620
5	28	5.3	529	2	A35366
6	24	4.6	530	2	S68200
7	23	4.4	523	2	SI1309
8	23	4.4	530	2	A48633
9	21	4.0	174	2	A47113
10	21	4.0	531	2	B47113
11	19	3.6	529	2	JN0200
12	18	3.4	530	2	C47113
13	18	3.4	530	2	S07390
14	17	3.2	530	2	S00163
15	14	2.7	530	2	A36276
16	14	2.7	530	2	A40467
17	11	2.1	531	2	A55788
18	10	1.9	508	2	T03910
19	10	1.9	529	2	A24600
20	10	1.9	531	2	A35343
21	10	1.9	531	2	T23835
22	10	1.9	535	2	I57961
23	9	1.7	434	2	D72353
24	9	1.7	530	2	JC5656
25	9	1.7	530	2	SI7512
26	9	1.7	531	2	B55788
27	9	1.7	531	2	A31340
28	9	1.7	533	2	A39092
29	8	1.5	44	2	B35704

Probes

30	8	1.5	98	1	FE8F2	ferredoxin [2Fe-2S
31	8	1.5	102	2	S20440	bilirubin UDP-gluc
32	8	1.5	285	2	G02240	UDP-glucuronosyltr
33	8	1.5	310	2	G02309	UDP-glucuronosyltr
34	8	1.5	342	2	T21530	hypothetical prote
35	8	1.5	381	1	A69784	macrolide glycosyl
36	8	1.5	407	2	T37104	probable glycosyl
37	8	1.5	412	2	T03517	probable dnaK-type
38	8	1.5	457	2	B84725	probable glucosylt
39	8	1.5	460	2	T00639	hypothetical prote
40	8	1.5	515	2	I40809	glutamyl-tRNA redu
41	8	1.5	541	2	JC5423	2-hydroxyacylsphn
42	8	1.5	541	2	A48801	2-hydroxyacylsphn
43	8	1.5	746	2	T01536	hypothetical prote
44	8	1.5	952	2	I50612	protein-tyrosine k
45	8	1.5	984	2	A39753	protein-tyrosine k

ALIGNMENTS

```
RESULT 1
SI5089
glucuronosyltransferase (EC 2.4.1.17) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C:Accession: SI5089
R:Lazard, D.; Zupko, K.; Porta, Y.; Nef, P.; Lazarevits, J.; Horn, S.; Khen, M.; Lanc
Nature 349, 790-793, 1991
A:Title: Odorant signal termination by olfactory UDP glucuronosyl transferase.
A:Reference number: SI5089; MID:91156050
A:Accession: SI5089
A:Molecule type: mRNA
A:Residues: 1-527 <LAZ>
A:Cross-references: GB:X57565; NID:g57762; PIDN:CAA40797.1; PID:g3980217
C:Superfamily: glucuronosyltransferase
C:Keywords: glucuronosyltransferase; hexosyltransferase

Query Match 7.6%; Score 40; DB 2; Length 527;
Best Local Similarity 100.0%; Pred. No. 9.1e-33;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 436 YKENAMRLSRHHDPVKPLDRAVFWIEFYMRHKGAKHLR 475
Db 436 YKENAMRLSRHHDPVKPLDRAVFWIEFYMRHKGAKHLR 475

RESULT 2
JN0619
glucuronosyltransferase (EC 2.4.1.17) 2B-4 precursor - human
N:Alternate names: UDP-glucuronosyltransferase 2B-11
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jun-2000
C:Accession: JN0619; A27878
R:Jin, C.J.; Miners, J.O.; Lillywhite, K.J.; Mackenzie, P.I.
Biochem. Biophys. Res. Commun. 194, 496-503, 1993
A:Title: cDNA cloning and expression of two new members of the human liver UDP-glucur
A:Reference number: JN0619; MID:93326164
A:Accession: JN0619
A:Molecule type: mRNA
A:Residues: 1-528 <JIN>
A:Cross-references: GB:AF081793; NID:g3426331
A:Experimental source: liver
R:Jackson, M.R.; McCarthy, L.R.; Harding, D.; Wilson, S.; Coughtrie, M.W.H.; Burchell
Biochem. J. 242, 581-588, 1987
A:Title: Cloning of a human liver microsomal UDP-glucuronosyltransferase cDNA.
A:Reference number: A27878; MID:87241362
A:Accession: A27878
A:Molecule type: mRNA
A:Residues: 1-108, 'F', '110-170', 'RP', '173-381', 'K', '383-384', 'SPR', '388-395', 'F', '397-528 <JAC
A:Cross-references: GB:I00317; NID:g37586; PIDN:CAA68415.1; PID:g37589
C:Genetics:
```

A:Gene: GDB:UGT2B4; UGT2B11
 A:Cross-references: GDB:5891331; OMIM:600067
 A:Map position: 4q13-4q13
 C:Superfamily: glucuronosyltransferase
 C:Keywords: glycoprotein; glucosyltransferase; hexosyltransferase; transmembrane protein
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-528/Product: glucuronosyltransferase 2B-11 #status predicted <MET>
 F:492-509/Domain: transmembrane #status predicted <TM>
 F:515/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match: 6.3%; Score 33; DB 2; Length 528;
 Best Local Similarity 100.0%; Pred. No. 1.6e-25;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 443 LSRHHDPVKPLDRAVFWIEFVMRHGAKHLR 475
 |||
 Db 445 LSRHHDPVKPLDRAVFWIEFVMRHGAKHLR 477

RESULT 3
 A42333
 glucuronosyltransferase (EC 2.4.1.17) 2 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 19-Jun-1992 #sequence-revision 18-Sep-1992 #text-change 29-Sep-1999
 C:Accession: A42233; A24324
 R:Mackenzie, P.I.; Roddoun, L.
 J. Biol. Chem. 265, 11328-11332, 1990
 A:Title: Organization of the rat UDP-glucuronosyltransferase, UDPGTR-2, gene and character
 A:Reference number: A42233; MUID:90293083
 A:Accession: A42233
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-529 <MAC>
 A:Cross-references: GB:J05482
 A:Note: the authors translated the codon GMA for residue 57 as B, and GNC for residue 11
 R:Mackenzie, P.I.
 J. Biol. Chem. 261, 6119-6125, 1986
 A:Title: Rat liver UDP-glucuronosyltransferase. Sequence and expression of a cDNA encodi
 A:Reference number: A24324; MUID:86196018
 A:Accession: A24324
 A:Molecule type: mRNA
 A:Residues: 1-407, 'V', 409-529 <MA2>
 A:Cross-references: GB:M3506; NID:9207580; PIDN:AAA42313.1; PID:9207581
 A:Experimental source: liver
 C:Superfamily: glucuronosyltransferase
 C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match: 5.5%; Score 29; DB 2; Length 529;
 Best Local Similarity 100.0%; Pred. No. 2.1e-21;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 435 SYKENAMRLSRHHDPVKPLDRAVFWIE 463
 |||
 Db 438 SYKENAMRLSRHHDPVKPLDRAVFWIE 466

RESULT 4
 JN0620
 UDP-glucuronosyltransferase (EC 2.4.1.-) 2B-10 precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 31-Dec-1993 #sequence-revision 31-Dec-1993 #text-change 28-May-1999
 C:Accession: JN0620
 R:Jin, C.J.; Miners, J.O.; Lillywhite, K.J.; Mackenzie, P.I.
 Biochem. Biophys. Res. Commun. 194, 496-503, 1993
 A:Title: cDNA cloning and expression of two new members of the human liver UDP-glucuron
 A:Reference number: JN0619; MUID:93326164
 A:Accession: JN0620
 A:Molecule type: mRNA
 A:Residues: 1-528 <JUN>
 A:Cross-references: GB:M6359; NID:9516149; PIDN:CAA44961.1; PID:9516150
 A:Experimental source: liver

C:Superfamily: glucuronosyltransferase
 C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase; transmembrane prot
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-528/Product: UDP-glucuronosyltransferase 2B-10 #status predicted <MET>
 F:491-508/Domain: transmembrane #status predicted <TM>
 F:66,314,481/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match: 5.3%; Score 28; DB 2; Length 528;
 Best Local Similarity 100.0%; Pred. No. 2.3e-20;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 448 HDQPVKPLDRAVFWIEFVMRHGAKHLR 475
 |||
 Db 449 HDQPVKPLDRAVFWIEFVMRHGAKHLR 476

RESULT 5
 A35366
 glucuronosyltransferase (EC 2.4.1.17) UDPGTR-2 precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 17-Aug-1990 #sequence-revision 17-Aug-1990 #text-change 29-Sep-1999
 C:Accession: A35366
 R:Ritter, J.K.; Sheen, Y.Y.; Owens, I.S.
 J. Biol. Chem. 265, 7900-7906, 1990
 A:Title: Cloning and expression of human liver UDP-glucuronosyltransferase in COS-1 c
 A:Reference number: A35366; MUID:90243659
 A:Accession: A35366
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-529 <KIT>
 A:Cross-references: GB:J05428; NID:9340079; PIDN:AAA36793.1; PID:9340080
 C:Genetics:
 A:Gene: GDB:UGT2B7; UGT2B9
 A:Cross-references: GDB:5892203; OMIM:600218
 A:Map position: 4q13-4q13
 C:Superfamily: glucuronosyltransferase
 C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match: 5.3%; Score 28; DB 2; Length 529;
 Best Local Similarity 100.0%; Pred. No. 2.3e-20;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 448 HDQPVKPLDRAVFWIEFVMRHGAKHLR 475
 |||
 Db 450 HDQPVKPLDRAVFWIEFVMRHGAKHLR 477

RESULT 6
 S68200
 glucuronosyltransferase (EC 2.4.1.17) precursor - rat
 N:Alternate names: UDP-glucuronosyltransferase
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 15-Feb-1997 #sequence-revision 13-Mar-1997 #text-change 17-Nov-2000
 C:Accession: S68200; A61266
 R:Green, M.D.; Clarke, D.J.; Oltun, E.M.; Styczynski, P.B.; Jackson, M.R.; Burchell,
 Arch. Biochem. Biophys. 322, 460-468, 1995
 A:Title: Cloning and expression of a rat liver phenobarbital-inducible UDP-glucuronos
 A:Reference number: S68200; MUID:96032689
 A:Accession: S68200
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-530 <GRE>
 A:Cross-references: EMBL:U06273; NID:9458394; PIDN:AAA3404.1; PID:9458395
 R:Styczynski, P.; Green, M.; Putig, J.; Coffman, B.; Tephly, T.
 Mol. Pharmacol. 40, 80-84, 1991
 A:Title: Purification and properties of a rat liver phenobarbital-inducible 4-hydroxy
 A:Reference number: A61266; MUID:91312327
 A:Accession: A61266
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 24-38 <STY>

C:Superfamily: glucuronosyltransferase
C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
F:1-23/Domain: signal sequence #status predicted <Sig>
F:24-530/Product: glucuronosyltransferase #status predicted <Mnt>

Query Match 4.6%; Score 24; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 3.1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 453 KPIDRAVFWIEFVMRHKGAKHLRS 476
|||||
DB 456 KPIDRAVFWIEFVMRHKGAKHLRS 479

RESULT 7
S11309
glucuronosyltransferase (EC 2.4.1.17) - human

A:Alternate names: estriol UDPglucuronosyltransferase

C:Species: Homo sapiens (man)

C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 29-Sep-1999

C:Accession: S11309

R:Coftman, B.L.; Tepfly, T.R.; Irshaid, Y.M.; Green, M.D.; Smith, C.; Jackson, M.R.; Woc Arch. Biochem. Biophys. 281, 170-175, 1990

A>Title: Characterization and primary sequence of a human hepatic microsomal estriol UDP-glucuronosyltransferase
A:Reference number: S11309; MUID:90343358

A:Accession: S11309

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-523 <COP>

A:Cross-references: GB:U06641; NID:g458398; PIDN:AA83406.1; PID:g458399

A>Note: the authors translated the codon AAG for residue 412 as Thr and ACC for residue

C:Superfamily: glucuronosyltransferase

C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 4.4%; Score 23; DB 2; Length 523;
Best Local Similarity 100.0%; Pred. No. 3.3e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 453 KPIDRAVFWIEFVMRHKGAKHLR 475
|||||
DB 449 KPIDRAVFWIEFVMRHKGAKHLR 471

RESULT 8
A48633

glucuronosyltransferase (EC 2.4.1.17) precursor - human

A:Alternate names: dihydrotestosterone/androstenediol UDP-glucuronosyltransferase isoform

C:Species: Homo sapiens (man)

C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 29-Sep-1999

C:Accession: A48633; I38559

R:Chen, F.; Rittner, J.K.; Wang, M.G.; McBride, O.W.; Lubet, R.A.; Owens, I.S. Biochemistry 32, 10648-10657, 1993

A>Title: Characterization of a cloned human dihydrotestosterone/androstenediol UDP-glucuronosyltransferase

A:Reference number: A48633; MUID:94002056

A:Accession: A48633

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-530 <CHS>

A:Experimental source: liver

A>Note: sequence extracted from NCBI backbone (NCBIP:138786)

R:Green, M.D.; Olturu, E.M.; Tepfly, T.R. Drug Metab. Dispos. 22, 799-805, 1994

A>Title: Stable expression of a human liver UDP-glucuronosyltransferase (UGT2B15) with a

A:Reference number: I38559; MUID:95136867

A:Accession: I38559

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-530 <RES>

A:Cross-references: EMBL:U08854; NID:g475758; PIDN:AAC50077.1; PID:g475759

C:Genetics:

A:Gene: GDB:UGT2B15; UGT2B8

A:Cross-references: GDB:5892418; OMIM:600219

A:Map position: 4q13-4q13

A:Superfamily: glucuronosyltransferase

C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 4.4%; Score 23; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 3.3e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 453 KPIDRAVFWIEFVMRHKGAKHLR 475
|||||
DB 456 KPIDRAVFWIEFVMRHKGAKHLR 478

RESULT 9
A47113
glucuronosyltransferase (EC 2.4.1.17), p-nitrophenol - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 13-Sep-1998

C:Accession: A47113

R:Tuke, R.H.; Pendurthi, U.R.; Nguyen, N.T.; Green, M.D.; Tepfly, T.R. J. Biol. Chem. 268, 15260-15266, 1993

A>Title: Cloning and characterization of rabbit liver UDP-glucuronosyltransferase CDN
A:Reference number: A47113; MUID:93315511

A:Accession: A47113

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-174 <TUK>

A:Superfamily: glucuronosyltransferase

C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 4.0%; Score 21; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 354 WIPONDLLGHPKTKAFTTHGG 374
|||||
DB 82 WIPONDLLGHPKTKAFTTHGG 102

RESULT 10
B47113

glucuronosyltransferase (EC 2.4.1.17) UGT2B13 precursor - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 29-Sep-1999

C:Accession: B47113

R:Tuke, R.H.; Pendurthi, U.R.; Nguyen, N.T.; Green, M.D.; Tepfly, T.R. J. Biol. Chem. 268, 15260-15266, 1993

A>Title: Cloning and characterization of rabbit liver UDP-glucuronosyltransferase CDN

A:Reference number: A47113; MUID:93315511

A:Accession: B47113

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-531 <TUK>

A:Cross-references: GB:I01081; NID:g165796; PIDN:AAA18020.1; PID:g165797

C:Superfamily: glucuronosyltransferase

C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 4.0%; Score 21; DB 2; Length 531;
Best Local Similarity 100.0%; Pred. No. 3.9e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 354 WIPONDLLGHPKTKAFTTHGG 374
|||||
DB 358 WIPONDLLGHPKTKAFTTHGG 378

RESULT 11
JF0200

orphan UDP-glucuronosyltransferase (EC 2.4.-.-) - human

N:Alternate names: UGT2B11
C:Species: Homo sapiens (man)
C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
C:Accession: J02000
R:Beaulieu, M.; Levesque, E.W.; Hum, D.; Belanger, A.
Biochem. Biophys. Res. Commun. 248, 44-50, 1998
A:Title: Isolation and characterization of a human orphan UDP-glucuronosyltransferase, U
A:Reference number: J02000; M01D:98340847
A:Accession: J02000
A:Molecule type: mRNA
A:Residues: 1-529 <BEA>
A:Cross-references: GB:AF016492
C:Comment: This enzyme catalyzes the transfer of glucuronic acid to a wide range of exog
C:Superfamily: glucuronosyltransferase
C:Keywords: glycoprotein; glycosyltransferase
F:493-509/Domain: membrane-anchoring #status predicted <MAC>
F:315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 3.6%; Score 19; DB 2; Length 529;
Best Local Similarity 100.0%; Pred. No. 4.5e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 448 HDOPVKPLDRAVWIEFVM 466
|||||
Db 450 HDOPVKPLDRAVWIEFVM 468

RESULT 12
C47113
glucuronosyltransferase (EC 2.4.1.17) UGT2B14 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 29-Sep-1999
C:Accession: C47113
R:Tukey, R.H.; Pendurthi, U.R.; Nguyen, N.T.; Green, M.D.; Tephly, T.R.
J. Biol. Chem. 268, 15260-15266, 1993
A:Title: Cloning and characterization of rabbit liver UDP-glucuronosyltransferase cDNAs.
A:Reference number: A47113; M01D:931511
A:Accession: C47113
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-530 <TUK>
A:Cross-references: GB:I01082; NID:gl65798; PIDN:AAA18021.1; PID:gl65799
C:Superfamily: glucuronosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 3.4%; Score 18; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. NO. 4.9e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 352 YDWIFQNDLGHPTKAP 369
|||||
Db 355 YDWIFQNDLGHPTKAP 372

RESULT 13
S07390
glucuronosyltransferase (EC 2.4.1.17) 3 precursor - rat
N:Alternate names: 17beta-hydroxysteroid UDP-glucuronosyltransferase; UDP-glucuronosyltr
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-May-1999
C:Accession: S07390; A3336; A28460; S59626
R:Harding, D.; Wilson, S.M.; Jackson, M.R.; Burchell, B.; Green, M.D.; Tephly, T.R.
Nucleic Acids Res. 15, 3936, 1987
A:Title: Nucleotide and deduced amino acid sequence of rat liver 17beta-hydroxysteroid
A:Reference number: S07390; M01D:87231096
A:Accession: S07390
A:Molecule type: mRNA
A:Residues: 1-530 <HAR>
A:Cross-references: EMBL:Y00156
A:Experimental source: liver
A:Accession: A3336

A:Molecule type: protein
A:Residues: 24-61 <HAR2>
A:Experimental source: liver
R:Mackenzie, P.I.
J. Biol. Chem. 262, 9744-9749, 1987
A:Title: Rat liver UDP-glucuronosyltransferase. Identification of cDNAs encoding two
A:Reference number: A28460; M01D:87250645
A:Accession: A28460
A:Molecule type: mRNA
A:Residues: 1-118, 'G', 120-240, 'L', 242-423, 'S', 425-499, 'T', 501-530 <MAC>
A:Experimental source: liver
R:Yamashita, A.; Watanabe, M.; Tonegawa, T.; Sugiyra, T.; Waku, K.
Biochem. J. 312, 301-308, 1995
A:Title: Acyl-CoA binding and acylation of UDP-glucuronosyltransferase isoforms of ra
A:Reference number: S59626; M01D:96077159
A:Accession: S59626
A:Molecule type: protein
A:Residues: 24-44 <YAM>
A:Experimental source: liver
C:Superfamily: glucuronosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-530/Product: glucuronosyltransferase #status experimental <MAT>
F:494-510/Domain: transmembrane #status predicted <TM>

Query Match 3.4%; Score 18; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 4.9e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 458 AVFWIEFVNRKGAHRL 475
|||||
Db 461 AVFWIEFVNRKGAHRL 478

RESULT 14
S00163
glucuronosyltransferase (EC 2.4.1.17) precursor - mouse
N:Alternate names: UDP-glucuronosyltransferase
C:Species: Mus musculus (house mouse)
C:Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 29-Sep-1999
C:Accession: S00163
R:Kimura, T.; Owens, I.S.
Eur. J. Biochem. 168, 515-521, 1987
A:Title: Mouse UDP-glucuronosyltransferase. cDNA and complete amino acid sequence and
A:Reference number: S00163; M01D:88029469
A:Accession: S00163
A:Molecule type: mRNA
A:Residues: 1-530 <KIM>
A:Cross-references: EMBL:X06358; NID:q55119; PIDN:CAA29657.1; PID:q55120
C:Comment: This enzyme catalyzes the conjugation of lipophilic compounds with glucuro
C:Superfamily: glucuronosyltransferase
C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase; transmembrane prot
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-530/Product: glucuronosyltransferase #status predicted <MAT>
F:494-510/Domain: transmembrane #status predicted <TM>
F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 3.2%; Score 17; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 5.3e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 453 KPLDRAVFWIEFVNRK 469
|||||
Db 456 KPLDRAVFWIEFVNRK 472

RESULT 15
A36276
glucuronosyltransferase (EC 2.4.1.17) 5 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 18-Jan-1991 #sequence_revision 13-Jan-1993 #text_change 29-Sep-1999

C:Accession: A36276
R:MacKenzie, P.I.
J. Biol. Chem. 265, 8699-8703, 1990
A:Title: The cDNA sequence and expression of a variant 17beta-hydroxysteroid UDP-glucuronosyltransferase
A:Reference number: A36276; MUID:90256795
A:Accession: A36276
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-530 <MAC>
A:Cross-references: GB:M33746; GB:J05440; NID:g207570; PIDN:AAA03217.1; PID:g207572
A:Note: the authors translated the codon GAG for residue 530 as Lys
C:Superfamily: glucuronosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 2.7%; Score 14; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 6.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PONDLLGHPKTKAF 369
DB 359 PONDLLGHPKTKAF 372

RESULT 16
A:Accession: A40467
glucuronosyltransferase (EC 2.4.1.17) precursor - rat
N:Alternate names: UDP-glucuronosyltransferase isoform 53K
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Feb-1992 #sequence_revision 07-Feb-1992 #text_change 17-Nov-2000
C:Accession: A40467; A23520; S59627; A26064; I55247
R:Haq, S.J.; Petersen, D.D.; Nebert, D.W.; MacKenzie, P.I.
DNA Cell Biol. 10, 515-524, 1991
A:Title: Isolation, sequence, and developmental expression of rat UGT2B2: the gene encoding UDP-glucuronosyltransferase
A:Reference number: A40467; MUID:91369480
A:Accession: A40467
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-530 <MAC>
R:Jackson, M.R.; Burchell, B.
Nucleic Acids Res. 14, 779-795, 1986
A:Title: The full length coding sequence of rat liver androsterone UDP-glucuronosyltransferase
A:Reference number: A23520; MUID:86120371
A:Accession: A23520
A:Molecule type: mRNA
A:Residues: 31-158, 'E', 160-285, 'S', 287-350, 'T', 352-362, 'I', 364-430, 'E', 432-530 <MAC>
A:Cross-references: GB:X03478; NID:g57452; PIDN:CAA27198.1; PID:g57453
A:Note: the authors translated the codon ATT for residue 321 as Asn
R:Yamashita, A.; Watanabe, M.; Tonegawa, T.; Sugitara, T.; Waku, K.
Biochem. J. 312, 301-308, 1995
A:Title: Acyl-CoA binding and acylation of UDP-glucuronosyltransferase isoforms of rat liver
A:Reference number: S59626; MUID:96077159
A:Accession: S59627
A:Molecule type: protein
A:Residues: 24-44 <YAM>
R:MacKenzie, P.I.
J. Biol. Chem. 261, 14112-14117, 1986
A:Title: Rat liver UDP-glucuronosyltransferase. cDNA sequence and expression of a form g
A:Reference number: A26064; MUID:87033594
A:Accession: A26064
A:Molecule type: mRNA
A:Residues: 1-430, 'E', 432-530 <MAC>
A:Cross-references: GB:J02589; NID:g207582; PIDN:AAA4214.1; PID:g207583
A:Experimental source: hepatic
C:Superfamily: glucuronosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-530/Product: glucuronosyltransferase #status experimental <MAT>

Query Match 2.7%; Score 14; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 6.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PONDLLGHPKTKAF 369
DB 359 PONDLLGHPKTKAF 372

RESULT 17
A:Accession: A55788
glucuronosyltransferase (EC 2.4.1.17) Ugt1.6 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 29-Sep-1999
C:Accession: A55788
R:Lamb, J.G.; Straub, P.; Tukey, R.H.
Biochemistry 33, 10513-10520, 1994
A:Title: Cloning and characterization of cDNAs encoding mouse Ugt1.6 and rabbit Ugt1.6
A:Reference number: A55788; MUID:94347791
A:Accession: A55788
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-531 <LAM>
A:Cross-references: GB:U09930; NID:g497941; PIDN:AAA51871.1; PID:g497942
C:Superfamily: glucuronosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 2.1%; Score 11; DB 2; Length 531;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PONDLLGHPKTKAF 369
DB 354 PONDLLGHPKTKAF 364

RESULT 18
A:Accession: T03910
UDP-glucuronosyltransferase homolog F39G3.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C:Accession: T03910
R:Du, Z.; Le, T.T.; Holmes, A.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid F39G3.
A:Reference number: Z15131
A:Accession: T03910
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-508 <DUZ>
A:Cross-references: EMBL:AF016424; NID:g2291203; PIDN:AA65327.1; PID:g2291205
C:Genetics:
A:Map position: V
A:Introns: 8/3; 49/1; 198/2; 229/3; 266/3; 359/3; 415/2
A:Note: F39G3.1
C:Superfamily: glucuronosyltransferase

Query Match 1.9%; Score 10; DB 2; Length 508;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 KTKAFTHGG 374
DB 345 KTKAFTHGG 354

RESULT 19
A:Accession: A24600
glucuronosyltransferase (EC 2.4.1.17) precursor, 3-methylcholanthrene-inducible - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 29-Sep-1999
C:Accession: A24600
R:Iyengar, T.; Hanlu, M.; Sogawa, K.; Fujii-Kuriyama, Y.; Watanabe, S.; Shively, J.E.
J. Biol. Chem. 261, 15607-15614, 1986

A:Title: Cloning and characterization of cDNA encoding 3-methylcholanthrene inducible rat
 A:Reference number: A24600; MUID:87057193
 A:Accession: A24600
 A:Molecule type: mRNA
 A:Residues: 1-529 <TYA>
 A:Cross-references: GB:J02612; NID:q207576; PIDN:AAA42311.1; PID:q207577
 A>Note: the authors translated the codon TAC for residue 168 as Phe and CTC for residue
 C:Superfamily: glucuronosyltransferase
 C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 1.9%; Score 10; DB 2; Length 529;
 Best Local Similarity 100.0%; Pred. No. 0.09;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 356 PONDLLGHPK 365
 |||||
 Db 352 PONDLLGHPK 361

RESULT 20

A35343
 glucuronosyltransferase (EC 2.4.1.17) - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 14-Sep-1990 #sequence_revision 14-Sep-1990 #text_change 29-Sep-1999
 C:Accession: A35343
 R:Sato, H.; Koiwai, O.; Tanabe, K.; Kashiwamata, S.
 Biochem. Biophys. Res. Commun. 169, 260-264, 1990
 A:Title: Isolation and sequencing of rat liver bilirubin UDP-glucuronosyltransferase cDN
 A:Reference number: A35343; MUID:90274676
 A:Accession: A35343
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-531 <SAT>
 A:Cross-references: GB:M34007; NID:q207578; PIDN:AAA42312.1; PID:q207579
 C:Superfamily: glucuronosyltransferase
 C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 1.9%; Score 10; DB 2; Length 531;
 Best Local Similarity 100.0%; Pred. No. 0.09;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 356 PONDLLGHPK 365
 |||||
 Db 354 PONDLLGHPK 363

RESULT 21

T23835
 hypothetical protein M88.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
 C:Accession: T23835
 R:Sulston, J.
 submitted to the EMBL Data Library, June 1994
 A:Reference number: Z19806
 A:Accession: T23835
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-531 <WIL>
 A:Cross-references: EMBL:Z34802; PIDN:CAA84336.1; GSPDB:GN00021; CESP:M88.1
 A:Experimental source: clone M88
 C:Genetics:
 A:Gene: CESP:M88.1
 A:Map position: 3
 A:Insertions: 30/3; 71/1; 220/2; 251/3; 288/3; 381/3; 437/2
 C:Superfamily: glucuronosyltransferase

Query Match 1.9%; Score 10; DB 2; Length 531;
 Best Local Similarity 100.0%; Pred. No. 0.09;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 365 KTKAFITGG 374
 |||||
 Db 367 KTKAFITGG 376

RESULT 22

157961
 glucuronosyltransferase (EC 2.4.1.17) precursor - rat
 N:Alternate names: glucuronosyltransferase 1 B1; morphine UGT
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 29-Sep-1999
 C:Accession: 157961; S51197; S68333
 R:Coffman, B.L.; Green, M.D.; King, C.D.; Teply, T.R.
 Moll. Pharmacol. 47, 1101-1105, 1995
 A:Title: Cloning and stable expression of a cDNA encoding a rat liver UDP-glucuronosy
 A:Reference number: 157961; MUID:95327065
 A:Accession: 157961
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-535 <RES>
 A:Cross-references: EMBL:U20551; NID:g695161; PIDN:AAC52219.1; PID:g695162
 R:Ishii, Y.; Tsuruda, K.; Tanaka, M.; Oguri, K.
 Arch. Biochem. Biophys. 315, 345-351, 1994
 A:Title: Purification of a phenobarbital-inducible morphine UDP-glucuronosyltransferase
 A:Reference number: S51197; MUID:95077409
 A:Accession: S51197
 A:Molecule type: protein
 A:Residues: 30-41 <ISH>
 R:Ikuhiro, S.; Eml, Y.; Iyanagi, T.
 Arch. Biochem. Biophys. 324, 267-272, 1995
 A:Title: Identification and analysis of drug-responsive expression of UDP-glucuronosy
 A:Reference number: S68333; MUID:96132654
 A:Accession: S68333
 A:Molecule type: protein
 A:Residues: 30-37 <IKU>
 C:Genetics:
 A:Gene: UGT1.1
 C:Superfamily: glucuronosyltransferase
 C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 1.9%; Score 10; DB 2; Length 535;
 Best Local Similarity 100.0%; Pred. No. 0.091;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 356 PONDLLGHPK 365
 |||||
 Db 358 PONDLLGHPK 367

RESULT 23

D72353
 lipopolysaccharide biosynthesis protein - Thermotoga maritima (strain MSB8)
 C:Species: Thermotoga maritima
 C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: D72353
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
 C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 A:Reference number: A72200; MUID:99287316
 A:Accession: D72353
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-434 <ARN>
 A:Cross-references: GB:AE001737; GB:AE000512; NID:g4981144; PIDN:AD35715.1; PID:g498
 A:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: TM0631

Query Match 1.7%; Score 9; DB 2; Length 434;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 RGHEVTVL 57
|||||
DB 43 RGHEVTVL 51

RESULT 24
UDP glucuronosyltransferase (EC 2.4.1.17) 1A10 precursor - human

C:Species: Homo sapiens (man)
C:Date: 17-Nov-1997 #sequence_revision 17-Nov-1997 #text_change 07-May-1999
C:Accession: J05656
R:Mojarrahi, B.; Mackenzie, P.I.
Biochem. Biophys. Res. Commun. 238, 775-778, 1997
A:Title: The human UDP glucuronosyltransferase, UGT1A10, glucuronidates mycophenolic acid
A:Reference number: J05656; MUID:97472286
A:Accession: J05656
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-530 <MO>

C:Comment: This enzyme plays a role in the elimination the antieoplastic and immunosuppre
C:Superfamily: glucuronosyltransferase
C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
F:1-25/Domain: signal sequence #status predicted <Sig>
F:488-504/Domain: transmembrane #status predicted <TM>
F:71,292,344/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.7%; Score 9; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GIVFSLGS 309
|||||
DB 298 GIVFSLGS 306

RESULT 25
glucuronosyltransferase (EC 2.4.1.17) - human

C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 29-Sep-1999
C:Accession: S17512
R:Wooster, R.; Sutherland, L.; Ebnner, T.; Clarke, D.; da Cruz e Silva, O.; Burchell, B.
Biochem. J. 278, 465-469, 1991
A:Title: Cloning and stable expression of a new member of the human liver phenol/bilirubi
A:Reference number: S17512; MUID:91378895
A:Accession: S17512
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-530 <MO>
A:Cross-references: GB:S55985; NID:q235453; PIDN:AA19791.1; PID:q235454
C:Superfamily: glucuronosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 1.7%; Score 9; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PONDILGHP 364
|||||
DB 353 PONDILGHP 361

RESULT 26
glucuronosyltransferase (EC 2.4.1.17) UGT1.6 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 29-Sep-1999

C:Accession: B55788
R:Lamb, J.G.; Strand, P.; Tukey, R.H.
Biochemistry 33, 10513-10520, 1994

A:Title: Cloning and characterization of cDNAs encoding mouse Ugt1.6 and rabbit Ugt1.
A:Reference number: A55788; MUID:94347791

A:Accession: B55788
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-531 <LAM>
A:Cross-references: GB:009030; NID:q483786; PIDN:AA51867.1; PID:q483787
C:Superfamily: glucuronosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 1.7%; Score 9; DB 2; Length 531;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GIVFSLGS 309
|||||
DB 300 GIVFSLGS 308

RESULT 27
A31340
glucuronosyltransferase (EC 2.4.1.17) UGT1A1 precursor - human

N:Alternate names: phenol transferase UGT1F
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 29-Sep-1999
C:Accession: A31340; A42586
R:Harding, D.; Fournel-Gigleux, S.; Jackson, M.R.; Burchell, B.
Proc. Natl. Acad. Sci. U.S.A. 85, 8381-8385, 1988
A:Title: Cloning and substrate specificity of a human phenol UDP-glucuronosyltransfer
A:Reference number: A31340; MUID:89042187
A:Accession: A31340
A:Molecule type: mRNA
A:Residues: 1-531 <HAR>

A:Cross-references: GB:J04093; NID:q624724; PIDN:AAA61251.1; PID:q624725
A:Note: the authors translated the codon TAC for residue 70 as Ser
R:Ritter, J.K.; Chen, F.; Sheen, Y.Y.; Tran, H.M.; Kimura, S.; Yeatman, M.T.; Owens, J.
J. Biol. Chem. 267, 3257-3261, 1992
A:Title: A novel complex locus UGT1 encodes human bilirubin, phenol, and other UDP-gl
A:Reference number: A42586; MUID:92147680
A:Accession: A42586
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-286 <RTT>

A:Note: sequence extracted from NCBI backbone (NCBIP:81457)
C:Genetics:
A:Gene: GDB:UGT1A1; UGT1
A:Cross-references: GDB:120007; OMIM:191740
A:Map position: 2q37-2q37
C:Superfamily: glucuronosyltransferase

C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 1.7%; Score 9; DB 2; Length 531;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GIVFSLGS 309
|||||
DB 299 GIVFSLGS 307

RESULT 28
A39092
glucuronosyltransferase (EC 2.4.1.17) 1 precursor, bilirubin-specific - human
N:Alternate names: bilirubin UDP-glucuronosyltransferase
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 29-Sep-1999
C:Accession: A39092; E42586; A48887
R:Ritter, J.K.; Crawford, J.M.; Owens, I.S.

J. Biol. Chem. 266, 1043-1047, 1991
 A>Title: Cloning of two human liver bilirubin UDP-glucuronosyltransferase cDNAs with ex
 A:Reference number: A39092; MUID:91093210
 A:Accession: A39092
 A:Molecule type: mRNA
 A:Residues: 1-533 <RI7>
 A:Cross-references: GB:M57899; NID:g184472; PIDN:AAA63195.1; PID:g184473
 R:Ritter, J.K.; Chen, F.; Shen, Y.Y.; Tran, H.M.; Kimura, S.; Yeatman, M.T.; Owens, I.S
 J. Biol. Chem. 267, 3257-3261, 1992
 A>Title: A novel complex locus ucgl encodes human bilirubin, phenol, and other UDP-gluc
 A:Reference number: A42586; MUID:92147660
 A:Accession: E42586
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-288 <RI2>
 A:Cross-references: GB:M84125; NID:g340131; PIDN:AAA61248.1; PID:g340132
 A>Note: sequence extracted from NCBI backbone (NCBIP:81433)
 R:Ritter, J.K.; Yeatman, M.T.; Kaiser, C.; Gridelli, B.; Owens, I.S.
 J. Biol. Chem. 268, 23573-23579, 1993
 A>Title: A phenylalanine codon deletion at the UGT1 gene complex locus of a Crigler-Naj
 A:Reference number: A48887; MUID:94043159
 A:Accession: A48887
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 161-170,172-180 <RI3>
 A:Experimental source: liver, Crigler-Najjar type I patient
 A>Note: sequence extracted from NCBI backbone (NCBIP:138934)
 C:Genetics:
 A:Gene: GDB:UGT1A1; UGT1
 A:Cross-references: GDB:120007; OMIM:191740
 A:Map position: 2q37-2q37
 C:Superfamily: glucuronosyltransferase
 C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 1.7%; Score 9; DB 2; Length 533;
 Best Local Similarity 100.0%; Pred. No. 0.97;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 GIVFSLGS 309
 |||||
 Db 301 GIVFSLGS 309

RESULT 29
 B35704
 glucuronosyltransferase (EC 2.4.1.17) - bovine (fragments)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 23-Jun-1993
 C:Accession: B35704
 R:Razard, D.; Tal, N.; Rudinstein, M.; Khen, M.; Lancet, D.; Zupko, K.
 Biochemistry 29, 7433-7440, 1990
 A>Title: Identification and biochemical analysis of novel olfactory-specific cytochrome
 A:Reference number: A35704; MUID:91027757
 A:Accession: B35704
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-44 <LA2>
 C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 1.5%; Score 8; DB 2; Length 44;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 322 IASALAQT 329
 |||||
 Db 24 IASALAQT 31

RESULT 30
 FEBF2
 ferredoxin [2Fe-2S] - yellow-green alga (Bumilleriopsis filiformis)

C:Species: Bumilleriopsis filiformis
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 13-Nov-1998
 C:Accession: A28857
 R:Inoue, K.; Hase, T.; Boeger, P.; Matsubara, H.
 J. Biochem. 94, 1451-1455, 1993
 A>Title: Amino acid sequence of a ferredoxin from Bumilleriopsis filiformis, a yellow
 A:Reference number: A28857; MUID:84087800
 A:Accession: A28857
 A:Molecule type: protein
 A:Residues: 1-98 <INO>
 A>Note: 1-Ala was also found
 C:Superfamily: ferredoxin [2Fe-2S]; ferredoxin [2Fe-2S] homology
 C:Keywords: 2Fe-2S; electron transfer; iron-sulfur protein; metalloprotein
 F:1-98/Product: ferredoxin [2Fe-2S] #status experimental <MAT>
 F:26-80/Domain: ferredoxin [2Fe-2S] homology <FER>
 F:41,46,49,79/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 1.5%; Score 8; DB 1; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 493 GFLITCYA 500
 |||||
 Db 74 GFLITCYA 81

RESULT 31
 S20440
 bilirubin UDP-glucuronosyltransferase - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
 C:Accession: S20440
 R:Clarke, D.J.; Keen, J.N.; Burchell, B.
 FEBS Lett. 299, 183-186, 1992
 A>Title: Isolation and characterisation of a new hepatic bilirubin UDP-glucuronosyltr
 A:Reference number: S20440; MUID:92183932
 A:Accession: S20440
 A:Molecule type: protein
 A:Residues: 1-102 <CLA>

Query Match 1.5%; Score 8; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 186 PAPLSYVP 193
 |||||
 Db 41 PAPLSYVP 48

RESULT 32
 G02240
 UDP-glucuronosyltransferase - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 29-Sep-1999
 C:Accession: G02240
 R:Owens, I.S.; Cho, J.W.; Gholami, N.; Porter, C.
 submitted to the EMBL Data Library, October 1995
 A:Reference number: G09343
 A:Accession: G02240
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-285 <OWE>
 A:Cross-references: EMBL:U39550; NID:g1051286; PIDN:AAA80547.1; PID:g1051287
 C:Genetics:
 A:Gene: UGT1J
 C:Superfamily: glucuronosyltransferase

Query Match 1.5%; Score 8; DB 2; Length 285;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 186 PAPLSTYP 193
|||||||
DB 184 PAPLSTYP 191

RESULT 33

UDP-glucuronosyltransferase - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 29-Sep-1999

C:Accession: G02309

R:Owens, I.S.; Cho, J.W.; Gholami, N.
submitted to the EMBL Data Library, December 1995

A:Reference number: H01030

A:Accession: G02309

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Cross-references: EMBL:U42604; NID:g1174043; PIDN:AAA86625.1; PID:g1174044

C:Genetics:

A:Gene: UGT1H

C:Superfamily: glucuronosyltransferase

Query Match 1.5%; Score 8; DB 2; Length 310;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 186 PAPLSTYP 193
|||||||
DB 184 PAPLSTYP 191

RESULT 34

hypothetical protein F28H7.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T21530

R:Berk, M.
submitted to the EMBL Data Library, May 1996

A:Reference number: Z19435

A:Accession: T21530

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-342 <MIL>

A:Cross-references: EMBL:Z72508; PIDN:CAA96641.1; GSPDB:GN00023; CESP:F28H7.1

A:Experimental source: clone F28H7

C:Genetics:

A:Gene: CESP:F28H7.1

A:Map position: 5

A:Introns: 63/3; 83/3; 148/3; 187/3; 278/2

Query Match 1.5%; Score 8; DB 2; Length 342;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 439 NAMRLSRI 446
|||||||
DB 192 NAMRLSRI 199

RESULT 35

macrolide glycosyltransferase homolog ydhe - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

C:Accession: A69784

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertet
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galluzzi, A.; Gal

iech, J.; Harwood, C.R.; Henault, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M

Koelter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau

Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl

A:Authors: Schleich, S.; Schreier, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis

A:Reference number: A69580; MUID:98044033

A:Accession: A69784

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-381 <KUN>

A:Cross-references: GB:Z99107; GB:AL009126; NID:g2632866; PIDN:CAB12391.1; PID:g26328

A:Experimental source: strain 168

C:Genetics:

A:Gene: ydhe

C:Superfamily: glycosyltransferase

Query Match 1.5%; Score 8; DB 1; Length 381;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 369 FITHGMN 376
|||||||
DB 281 FITHGMN 288

RESULT 36

probable glycosyl transferase - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000

C:Accession: T37104

R:Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream,
submitted to the EMBL Data Library, August 1999

A:Reference number: Z21588

A:Accession: T37104

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-407 <SAU>

A:Cross-references: EMBL:AL109950; PIDN:CAB52955.1; GSPDB:GN00070; SCOEDB:SCJ4.21

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SCJ4.21

C:Superfamily: glycosyltransferase

Query Match 1.5%; Score 8; DB 2; Length 407;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 369 FITHGMN 376
|||||||
DB 294 FITHGMN 301

RESULT 37

probable dnaK-type molecular chaperone - Rhodobacter capsulatus

C:Species: Rhodobacter capsulatus

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999

C:Accession: T03517

R:Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fomstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997

A:Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SBI

A:Reference number: Z14955; MUID:97404404

A:Accession: T03517

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-412 <VIC>
A:Cross-references: EMBL:AF010496; NID:g3128256; PIDN:AAC16170.1; PID:g3128318
C:Genetics:
A:Map position: 1
C:Keywords: heat shock; molecular chaperone

Query Match 1.5%; Score 8; DB 2; Length 412;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 87 NEIFVDLA 94
|||||
Db 245 NEIFVDLA 252

RESULT 38
B84725
Probable glucosyltransferase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: B84725

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Koffel, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: B84725

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-457 <STO>
A:Cross-references: GB:AE002093; NID:g4887757; PIDN:AA032293.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g31790
A:Map position: 2
C:Superfamily: flavonol O3-glucosyltransferase

Query Match 1.5%; Score 8; DB 2; Length 457;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 385 GVPWGV 392
|||||
Db 366 GVPWGV 373

RESULT 39
T00639
hypothetical protein F316.2 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 24-Nov-1999
C:Accession: T00639

R:Federspiel, N.A.; Palm, C.J.; Conway, A.B.; Kurtz, D.B.; Conway, A.R.; Au, M.; Araujo,
; Vysotskaya, V.S.; Yu, G.; Ecker, J.; Theologis, A.; Davis, R.W.
submitted to the EMBL Data Library, February 1998
A:Reference number: 214197
A:Accession: T00639

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-460 <FED>
A:Cross-references: EMBL:AC002396; NID:g2749918; PID:g2829862; GSPDB:GN00059; ATSP:F316.
C:Genetics:
A:Gene: ATSP:F316.2
A:Map position: 1
A:Introns: 219/3
C:Superfamily: flavonol O3-glucosyltransferase

Query Match 1.5%; Score 8; DB 2; Length 460;

Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 385 GVPWGV 392
|||||
Db 367 GVPWGV 374

RESULT 40
I40809
glutamyl-tRNA reductase (EC 1.2.1.-) - Clostridium josui
C:Species: Clostridium josui
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 15-Oct-1999
C:Accession: I40809

R:Fujino, E.; Fujino, T.; Karita, S.; Sakka, K.; Ohmiya, K.
J. Bacteriol. 177, 5169-5175, 1995
A:Title: Cloning and sequencing of some genes responsible for porphyrin biosynthesis
A:Reference number: A57344; MUID:95394829
A:Accession: I40809

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-515 <RES>
A:Cross-references: GB:D28503; NID:g536874; PIDN:BAA05860.1; PID:g536875
C:Genetics:
A:Gene: hema
C:Keywords: oxidoreductase

Query Match 1.5%; Score 8; DB 2; Length 515;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 88 EIFVDLAL 95
|||||
Db 285 EIFVDLAL 292

RESULT 41
JC5423
2-hydroxyacylsphingosine 1-beta-galactosyltransferase (EC 2.4.1.45) - human
N:Alternate names: UDP-galactose:ceramide galactosyltransferase
C:Species: Homo sapiens (man)
C:Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 26-Aug-1999
C:Accession: JC5423
R:Kapitonov, D.; Yu, R.K.
Biochem. Biophys. Res. Commun. 232, 449-453, 1997
A:Title: Cloning, characterization, and expression of human ceramide galactosyltransf
A:Reference number: JC5423; MUID:97242209
A:Accession: JC5423
A:Molecule type: mRNA
A:Residues: 1-541 <KAP>
A:Cross-references: GB:U62899
A:Experimental source: fetal glioma cell
C:Comment: This enzyme catalyzes the final step of galactosylceramide synthesis.
C:Genetics:
A:Gene: cgt

C:Superfamily: glucuronosyltransferase
C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
F:472-492/Domains: hydrophobic #status predicted <HYD>
F:538-540/Region: endoplasmic reticulum retention signal #status atypical
F:78,333,442/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.5%; Score 8; DB 2; Length 541;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 356 PONDLLGH 363
|||||
Db 342 PONDLLGH 349

RESULT 42

A48801
 2-hydroxyacylsphingosine 1-beta-galactosyltransferase (EC 2.4.1.45) precursor - rat
 N:Alternate names: UDPgalactose-ceramide galactosyltransferase
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C:Accession: A48801; 156576; S63480
 R:Schulte, S.; Stoffel, W.
 Proc. Natl. Acad. Sci. U.S.A. 90, 10265-10269, 1993
 A:Title: Ceramide UDPgalactosyltransferase from myelinating rat brain: purification, cDNA
 A:Reference number: A48801; MUID:94052143
 A:Accession: A48801
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-541 <SCH>
 A:Cross-references: GB:L21698; NID:9437665; PIDN:AAA16108.1; PID:9437666
 A:Experimental source: brain
 A:Note: sequence extracted from NCBI backbone (NCBIN:139520, NCBI:139522)
 R:Stahl, N.; Jurevics, H.; Morell, P.; Suzuki, K.; Popko, B.
 J. Neurosci. Res. 38, 234-242, 1994
 A:Title: Isolation, characterization, and expression of cDNA clones that encode rat UDP-
 A:Reference number: 156576; MUID:94358923
 A:Accession: 156576
 A:Status: preliminary
 A:Molecule type: translated from GB/EMBL/DBJ
 A:Residues: 1-541 <RES>
 A:Cross-references: EMBL:U07683; NID:9464025; PIDN:AAA50212.1; PID:9464026
 R:Schulte, S.; Stoffel, W.
 Eur. J. Biochem. 233, 947-953, 1995
 A:Title: UDP galactose:ceramide galactosyltransferase and glutamate/aspartate transport
 A:Reference number: S63480; MUID:96085162
 A:Accession: S63480
 A:Molecule type: protein
 A:Residues: 21-28, 'A', 30-31, 'Q', 33-39; 73-77, 'X', 79-87; 155-166, 'Q', 168-173; 315-322; 330-33
 A:Experimental source: brain
 C:Function:
 A:Description: transfers galactose from UDP-galactose to ceramide
 C:Superfamily: glucuronosyltransferase
 C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
 F:1-20/Domain: signal sequence #status predicted <SID>
 F:21-541/Product: 2-hydroxyacylsphingosine 1-beta-galactosyltransferase #status experime
 F:78,333/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 1.5%; Score 8; DB 2; Length 541;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PONDILGH 363
 DB 342 PONDILGH 349

RESULT 43
 T01536
 hypothetical protein A.IG005110.20 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 24-Mar-1999
 C:Accession: T01536
 R:Andrews, S.
 submitted to the EMBL Data Library, July 1997
 A:Description: The sequence of A. thaliana IG005110.
 A:Reference number: 214347
 A:Accession: T01536
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-746 <AND>
 A:Cross-references: EMBL:AF013293; NID:92252823; PID:92252840
 A:Experimental source: cultivar Columbia
 C:Genetics:
 A:Map position: 4
 A:Introns: 143/3; 352/2; 469/3; 505/1
 A:Note: A_IG005110.20

Query Match 1.5%; Score 8; DB 2; Length 746;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 VFSLGSLF 311
 DB 715 VFSLGSLF 722

RESULT 44
 I50612
 protein-tyrosine kinase (EC 2.7.1.112) Cdk6 - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 04-Feb-2000
 C:Accession: I50612; S33503
 R:Sajjadi, F.G.; Pasquale, E.B.
 Oncogene 8, 1807-1813, 1993
 A:Title: Five novel avian Epi-related tyrosine kinases are differentially expressed.
 A:Reference number: I50611; MUID:93288394
 A:Accession: I50612
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-952 <SAJ>
 A:Cross-references: EMBL:U19110; NID:9312901; PIDN:CAA79526.1; PID:9312902
 C:Genetics:
 A:Gene: Cdk6
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
 C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein
 F:585-853/Domain: protein kinase homology <KIN>
 F:593-601/Region: protein kinase ATP-binding motif
 F:876-942/Domain: SAM homology <SAM>

Query Match 1.5%; Score 8; DB 2; Length 952;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 MTSEDLR 425
 DB 914 MTSEDLR 921

RESULT 45
 A39753
 protein-tyrosine kinase (EC 2.7.1.112) elk precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 04-Feb-2000
 C:Accession: A39753; S04327
 R:Luhotak, V.; Greer, P.; Letwin, K.; Pawson, T.
 Mol. Cell. Biol. 11, 2496-2502, 1991
 A:Title: Characterization of elk, a brain-specific receptor tyrosine kinase.
 A:Reference number: A39753; MUID:91203869
 A:Accession: A39753
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-984 <LHO>
 A:Cross-references: GB:M59814
 R:Letwin, K.; Yee, S.P.; Pawson, T.
 Oncogene 3, 621-627, 1988
 A:Title: Novel protein-tyrosine kinase cDNAs related to fps/fes and eph cloned using
 A:Reference number: S04327; MUID:94167102
 A:Accession: S04327
 A:Molecule type: mRNA
 A:Residues: 605-984 <LET>
 A:Cross-references: EMBL:X13411; NID:956094; PIDN:CAA3177.1; PID:956095
 C:Genetics:
 A:Gene: elk
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
 C:Keywords: ATP; autophosphorylation; kinase-related transforming protein; phosphopro
 F:617-885/Domain: protein kinase homology <KIN>
 F:625-633/Region: protein kinase ATP-binding motif
 F:908-974/Domain: SAM homology <SAM>

Query Match	1.58;	Score 8;	DB 2;	Length 984;
Best Local Similarity	100.0%;	Pred. No. 18;		
Matches	8;	Conservative	0;	Mismatches
Oy	418	MTSEDLR	425	
Db	946	MTSEDLR	953	

Search completed: August 13, 2001, 13:44:29
 Job time: 259 sec